

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: MARUTA, Kazuhiko
KUBOTA, Michio
SUGIMOTO, Toshiyuki
- (ii) TITLE OF INVENTION: RECOMBINANT THERMOSTABLE ENZYME WHICH
FORMS NON-REDUCING SACCHARIDE FROM REDUCING AMYLACEOUS
SACCHARIDE
- (iii) NUMBER OF SEQUENCES: 18
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Browdy and Neimark
(B) STREET: 419 Seventh Street N.W. Ste. 300
(C) CITY: Washington
(D) STATE: D.C.
(E) COUNTRY: U.S.A.
(F) ZIP: 20004
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US
(B) FILING DATE: 21-JUL-1994
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: JP 190183/1994
(B) FILING DATE: 21-JUL-1994
- (viii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: JP Not yet received
(B) FILING DATE: 04-JUL-1995
- (ix) ATTORNEY/AGENT INFORMATION:
(A) NAME: Browdy, Roger L.
(B) REGISTRATION NUMBER: 25,618
(C) REFERENCE/DOCKET NUMBER: MARUTA=3
- (x) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (202) 628-5197
(B) TELEFAX: (202) 737-3528

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 720 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Val Ile Ser Ala Thr Tyr Arg Leu Gln Leu Asn Lys Asn Phe Asn Phe
1 5 10 15

Gly Asp Val Ile Asp Asn Leu Trp Tyr Phe Lys Asp Leu Gly Val Ser
 20 25 30
 His Leu Tyr Leu Ser Pro Val Leu Met Ala Ser Pro Gly Ser Asn His
 35 40 45
 Gly Tyr Asp Val Ile Asp His Ser Arg Ile Asn Asp Glu Leu Gly Gly
 50 55 60
 Glu Lys Glu Tyr Arg Arg Leu Ile Glu Thr Ala His Thr Ile Gly Leu
 65 70 75 80
 Gly Ile Ile Gln Asp Ile Val Pro Asn His Met Ala Val Asn Ser Leu
 85 90 95
 Asn Trp Arg Leu Met Asp Val Leu Lys Met Gly Lys Lys Ser Lys Tyr
 100 105 110
 Tyr Thr Tyr Phe Asp Phe Phe Pro Glu Asp Asp Lys Ile Arg Leu Pro
 115 120 125
 Ile Leu Gly Glu Asp Leu Asp Thr Val Ile Ser Lys Gly Leu Leu Lys
 130 135 140
 Ile Val Lys Asp Gly Asp Glu Tyr Phe Leu Glu Tyr Phe Lys Trp Lys
 145 150 155 160
 Leu Pro Leu Thr Glu Val Gly Asn Asp Ile Tyr Asp Thr Leu Gln Lys
 165 170 175
 Gln Asn Tyr Thr Leu Met Ser Trp Lys Asn Pro Pro Ser Tyr Arg Arg
 180 185 190
 Phe Phe Asp Val Asn Thr Leu Ile Gly Val Asn Val Glu Lys Asp His
 195 200 205
 Val Phe Gln Glu Ser His Ser Lys Ile Leu Asp Leu Asp Val Asp Gly
 210 215 220
 Tyr Arg Ile Asp His Ile Asp Gly Leu Tyr Asp Pro Glu Lys Tyr Ile
 225 230 235 240
 Asn Asp Leu Arg Ser Ile Ile Lys Asn Lys Ile Ile Ile Val Glu Lys
 245 250 255
 Ile Leu Gly Phe Gln Glu Glu Leu Lys Leu Asn Ser Asp Gly Thr Thr
 260 265 270
 Gly Tyr Asp Phe Leu Asn Tyr Ser Asn Leu Leu Phe Asn Phe Asn Gln
 275 280 285
 Glu Ile Met Asp Ser Ile Tyr Glu Asn Phe Thr Ala Glu Lys Ile Ser
 290 295 300
 Ile Ser Glu Ser Ile Lys Lys Ile Lys Ala Gln Ile Ile Asp Glu Leu
 305 310 315 320
 Phe Ser Tyr Glu Val Lys Arg Leu Ala Ser Gln Leu Gly Ile Ser Tyr
 325 330 335
 Asp Ile Leu Arg Asp Tyr Leu Ser Cys Ile Asp Val Tyr Arg Thr Tyr
 340 345 350
 Ala Asn Gln Ile Val Lys Glu Cys Asp Lys Thr Asn Glu Ile Glu Glu
 355 360 365

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Ala Thr Lys Arg Asn Pro Glu Ala Tyr Thr Lys Leu Gln Gln Tyr Met
 370 375 380
 Pro Ala Val Tyr Ala Lys Ala Tyr Glu Asp Thr Phe Leu Phe Arg Tyr
 385 390 395 400
 Asn Arg Leu Ile Ser Ile Asn Glu Val Gly Ser Asp Leu Arg Tyr Tyr
 405 410 415
 Lys Ile Ser Pro Asp Gln Phe His Val Phe Asn Gln Lys Arg Arg Gly
 420 425 430
 Lys Ile Thr Leu Asn Ala Thr Ser Thr His Asp Thr Lys Phe Ser Glu
 435 440 445
 Asp Val Arg Met Lys Ile Ser Val Leu Ser Glu Phe Pro Glu Glu Trp
 450 455 460
 Lys Asn Lys Val Glu Glu Trp His Ser Ile Ile Asn Pro Lys Val Ser
 465 470 475 480
 Arg Asn Asp Glu Tyr Arg Tyr Tyr Gln Val Leu Val Gly Ser Phe Tyr
 485 490 495
 Glu Gly Phe Ser Asn Asp Phe Lys Glu Arg Ile Lys Gln His Met Ile
 500 505 510
 Lys Ser Val Arg Glu Ala Lys Ile Asn Thr Ser Trp Arg Asn Gln Asn
 515 520 525
 Lys Glu Tyr Glu Asn Arg Val Met Glu Leu Val Glu Glu Thr Phe Thr
 530 535 540
 Asn Lys Asp Phe Ile Lys Ser Phe Met Lys Phe Glu Ser Lys Ile Arg
 545 550 555 560
 Arg Ile Gly Met Ile Lys Ser Leu Ser Leu Val Ala Leu Lys Ile Met
 565 570 575
 Ser Ala Gly Ile Pro Asp Phe Tyr Gln Gly Thr Glu Ile Trp Arg Tyr
 580 585 590
 Leu Leu Thr Asp Pro Asp Asn Arg Val Pro Val Asp Phe Lys Lys Leu
 595 600 605
 His Glu Ile Leu Glu Lys Ser Lys Lys Phe Glu Lys Asn Met Leu Glu
 610 615 620
 Ser Met Asp Asp Gly Arg Ile Lys Met Tyr Leu Thr Tyr Lys Leu Leu
 625 630 635 640
 Ser Leu Arg Lys Gln Leu Ala Glu Asp Phe Leu Lys Gly Glu Tyr Lys
 645 650 655
 Gly Leu Asp Leu Glu Glu Gly Leu Cys Gly Phe Ile Arg Phe Asn Lys
 660 665 670
 Ile Leu Val Ile Ile Lys Thr Lys Gly Ser Val Asn Tyr Lys Leu Lys
 675 680 685
 Leu Glu Glu Gly Ala Ile Tyr Thr Asp Val Leu Thr Gly Glu Glu Ile
 690 695 700
 Lys Lys Glu Val Gln Ile Asn Glu Leu Pro Arg Ile Leu Val Arg Met
 705 710 715 720

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTGATATCAG CAACCTACAG ATTACAGTTA AATAAGAATT TTAATTTTGG TGACGTAATC 60
GATAACCTAT GGTATTTTAA GGATTTAGGA GTTTCCTATC TCTACCTCTC TCCTGTCTTA 120
ATGGCTTCGC CAGGAAGTAA CCATGGGTAC GATGTAATAG ATCATTCAAG GATAAACGAT 180
GAACTTGGAG GAGAGAAAGA ATACAGGAGA TTAATAGAGA CAGCTCATAC TATTGGATTA 240
GGTATTATAC AGGACATAGT ACCAAATCAC ATGGCTGTAA ATTCTCTAAA TTGGCGACTA 300
ATGGATGTAT TAAAAATGGG TAAAAAGAGT AAATATTATA CGTACTTTGA CTTTTTCCCA 360
GAAGATGATA AGATACGATT ACCCATATTA GGAGAAGATT TAGATACAGT GATAAGTAAA 420
GGTTTATTAA AGATAGTAAA AGATGGAGAT GAATATTTCC TAGAATATTT CAAATGGAAA 480
CTTCCTCTAA CAGAGGTTGG AAATGATATA TACGACACTT TACAAAAACA GAATTATACC 540
CTAATGTCTT GGAAAAATCC TCCTAGCTAT AGACGATTCT TCGATGTTAA TACTTTAATA 600
GGAGTAAATG TCGAAAAAGA TCACGTATTT CAAGAGTCCC ATTCAAAGAT CTTAGATTTA 660
GATGTTGATG GCTATAGAAT TGATCATATT GATGGATTAT ATGATCCTGA GAAATATATT 720
AATGACCTGA GGTCAATAAT TAAAAATAAA ATAATTATTG TAGAAAAAAT TCTGGGATTT 780
CAGGAGGAAT TAAAATTAAA TTCAGATGGA ACTACAGGAT ATGACTTCTT AAATTACTCC 840
AACTTACTGT TTAATTTTAA TCAAGAGATA ATGGACAGTA TATATGAGAA TTTCACAGCG 900
GAGAAAATAT CTATAAGTGA AAGTATAAAG AAAATAAAAG CGCAAATAAT TGATGAGCTA 960
TTTAGTTATG AAGTTAAAAG ATTAGCATCA CAACTAGGAA TTAGCTACGA TATATTGAGA 1020
GATTACCTTT CTTGTATAGA TGTGTACAGA ACTTATGCTA ATCAGATTGT AAAAGAGTGT 1080
GATAAGACCA ATGAGATAGA GGAAGCAACC AAAAGAAATC CAGAGGCTTA TACTAAATTA 1140
CAACAATATA TGCCAGCAGT ATACGCTAAA GCTTATGAAG ATACTTTCCT CTTTAGATAC 1200
AATAGATTAA TATCCATAAA TGAGGTTGGA AGCGATTTAC GATATTATAA GATATCGCCT 1260
GATCAGTTTC ATGTATTTAA TCAAAAACGA AGAGGAAAAA TCACACTAAA TGCCACTAGC 1320
ACACATGATA CTAAGTTTAG TGAAGATGTA AGGATGAAAA TAAGTGTATT AAGTGAATTT 1380
CCTGAAGAAT GGAAAAATAA GGTCGAGGAA TGGCATAGTA TCATAAATCC AAAGGTATCA 1440
AGAAATGATG AATATAGATA TTATCAGGTT TTAGTGGGAA GTTTTTATGA GGGATTCTCT 1500
AATGATTTTA AGGAGAGAAT AAAGCAACAT ATGATAAAAA GTGTCAGAGA AGCTAAGATA 1560
AATACCTCAT GGAGAAATCA AAATAAGAA TATGAAAATA GAGTAATGGA ATTAGTGGAA 1620

GAAACTTTTA CCAATAAGGA TTTCATTAAA AGTTTCATGA AATTTGAAAG TAAGATAAGA 1680
 AGGATAGGGA TGATTAAGAG CTTATCCTTG GTCGCATTAA AAATTATGTC AGCCGGTATA 1740
 CCTGATTTTT ATCAGGGAAC AGAAATATGG CGATATTTAC TTACAGATCC AGATAACAGA 1800
 GTCCCACTGG ATTTTAAGAA ATTACACGAA ATATTAGAAA AATCCAAAAA ATTTGAAAAA 1860
 AATATGTTAG AGTCTATGGA CGATGGAAGA ATTAAGATGT ATTTAACATA TAAGCTTTTA 1920
 TCCCTAAGAA AACAGTTGGC TGAGGATTTT TTAAAGGGCG AGTATAAGGG ATTAGATCTA 1980
 GAAGAAGGAC TATGTGGGTT TATTAGGTTT AACAAAATTT TGGTAATAAT AAAAACCAAG 2040
 GGAAGTGTTA ATTACAACT GAAACTTGAA GAGGGAGCAA TTTACACAGA TGTATTGACA 2100
 GGAGAAGAAA TTAAAAAGA GGTACAGATT AATGAGCTAC CTAGGATACT AGTTAGAATG 2160

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Ile	Ser	Ala	Thr	Tyr	Arg	Leu	Gln	Leu	Asn	Lys	Asn	Phe	Asn	Phe
1				5				10					15		
Gly	Asp	Val	Ile	Asp	Asn	Leu	Trp	Tyr	Phe	Lys	Asp	Leu	Gly		
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Val	Glu	Glu	Trp	His	Ser	Ile	Ile	Asn	Pro	Lys
1				5					10	

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2160 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTG ATA TCA GCA ACC TAC AGA TTA CAG TTA AAT AAG AAT TTT AAT TTT Val Ile Ser Ala Thr Tyr Arg Leu Gln Leu Asn Lys Asn Phe Asn Phe 1 5 10 15	48
GGT GAC GTA ATC GAT AAC CTA TGG TAT TTT AAG GAT TTA GGA GTT TCC Gly Asp Val Ile Asp Asn Leu Trp Tyr Phe Lys Asp Leu Gly Val Ser 20 25 30	96
CAT CTC TAC CTC TCT CCT GTC TTA ATG GCT TCG CCA GGA AGT AAC CAT His Leu Tyr Leu Ser Pro Val Leu Met Ala Ser Pro Gly Ser Asn His 35 40 45	144
GGG TAC GAT GTA ATA GAT CAT TCA AGG ATA AAC GAT GAA CTT GGA GGA Gly Tyr Asp Val Ile Asp His Ser Arg Ile Asn Asp Glu Leu Gly Gly 50 55 60	192
GAG AAA GAA TAC AGG AGA TTA ATA GAG ACA GCT CAT ACT ATT GGA TTA Glu Lys Glu Tyr Arg Arg Leu Ile Glu Thr Ala His Thr Ile Gly Leu 65 70 75 80	240
GGT ATT ATA CAG GAC ATA GTA CCA AAT CAC ATG GCT GTA AAT TCT CTA Gly Ile Ile Gln Asp Ile Val Pro Asn His Met Ala Val Asn Ser Leu 85 90 95	288
AAT TGG CGA CTA ATG GAT GTA TTA AAA ATG GGT AAA AAG AGT AAA TAT Asn Trp Arg Leu Met Asp Val Leu Lys Met Gly Lys Lys Ser Lys Tyr 100 105 110	336
TAT ACG TAC TTT GAC TTT TTC CCA GAA GAT GAT AAG ATA CGA TTA CCC Tyr Thr Tyr Phe Asp Phe Phe Pro Glu Asp Asp Lys Ile Arg Leu Pro 115 120 125	384
ATA TTA GGA GAA GAT TTA GAT ACA GTG ATA AGT AAA GGT TTA TTA AAG Ile Leu Gly Glu Asp Leu Asp Thr Val Ile Ser Lys Gly Leu Leu Lys 130 135 140	432
ATA GTA AAA GAT GGA GAT GAA TAT TTC CTA GAA TAT TTC AAA TGG AAA Ile Val Lys Asp Gly Asp Glu Tyr Phe Leu Glu Tyr Phe Lys Trp Lys 145 150 155 160	480
CTT CCT CTA ACA GAG GTT GGA AAT GAT ATA TAC GAC ACT TTA CAA AAA Leu Pro Leu Thr Glu Val Gly Asn Asp Ile Tyr Asp Thr Leu Gln Lys 165 170 175	528
CAG AAT TAT ACC CTA ATG TCT TGG AAA AAT CCT CCT AGC TAT AGA CGA Gln Asn Tyr Thr Leu Met Ser Trp Lys Asn Pro Pro Ser Tyr Arg Arg 180 185 190	576
TTC TTC GAT GTT AAT ACT TTA ATA GGA GTA AAT GTC GAA AAA GAT CAC Phe Phe Asp Val Asn Thr Leu Ile Gly Val Asn Val Glu Lys Asp His 195 200 205	624
GTA TTT CAA GAG TCC CAT TCA AAG ATC TTA GAT TTA GAT GTT GAT GGC Val Phe Gln Glu Ser His Ser Lys Ile Leu Asp Leu Asp Val Asp Gly 210 215 220	672
TAT AGA ATT GAT CAT ATT GAT GGA TTA TAT GAT CCT GAG AAA TAT ATT Tyr Arg Ile Asp His Ile Asp Gly Leu Tyr Asp Pro Glu Lys Tyr Ile 225 230 235 240	720
AAT GAC CTG AGG TCA ATA ATT AAA AAT AAA ATA ATT ATT GTA GAA AAA Asn Asp Leu Arg Ser Ile Ile Lys Asn Lys Ile Ile Ile Val Glu Lys 245 250 255	768
ATT CTG GGA TTT CAG GAG GAA TTA AAA TTA AAT TCA GAT GGA ACT ACA Ile Leu Gly Phe Gln Glu Glu Leu Lys Leu Asn Ser Asp Gly Thr Thr 260 265 270	816

GGA TAT GAC TTC TTA AAT TAC TCC AAC TTA CTG TTT AAT TTT AAT CAA Gly Tyr Asp Phe Leu Asn Tyr Ser Asn Leu Leu Phe Asn Phe Asn Gln 275 280 285	864
GAG ATA ATG GAC AGT ATA TAT GAG AAT TTC ACA GCG GAG AAA ATA TCT Glu Ile Met Asp Ser Ile Tyr Glu Asn Phe Thr Ala Glu Lys Ile Ser 290 295 300	912
ATA AGT GAA AGT ATA AAG AAA ATA AAA GCG CAA ATA ATT GAT GAG CTA Ile Ser Glu Ser Ile Lys Lys Ile Lys Ala Gln Ile Ile Asp Glu Leu 305 310 315 320	960
TTT AGT TAT GAA GTT AAA AGA TTA GCA TCA CAA CTA GGA ATT AGC TAC Phe Ser Tyr Glu Val Lys Arg Leu Ala Ser Gln Leu Gly Ile Ser Tyr 325 330 335	1008
GAT ATA TTG AGA GAT TAC CTT TCT TGT ATA GAT GTG TAC AGA ACT TAT Asp Ile Leu Arg Asp Tyr Leu Ser Cys Ile Asp Val Tyr Arg Thr Tyr 340 345 350	1056
GCT AAT CAG ATT GTA AAA GAG TGT GAT AAG ACC AAT GAG ATA GAG GAA Ala Asn Gln Ile Val Lys Glu Cys Asp Lys Thr Asn Glu Ile Glu Glu 355 360 365	1104
GCA ACC AAA AGA AAT CCA GAG GCT TAT ACT AAA TTA CAA CAA TAT ATG Ala Thr Lys Arg Asn Pro Glu Ala Tyr Thr Lys Leu Gln Gln Tyr Met 370 375 380	1152
CCA GCA GTA TAC GCT AAA GCT TAT GAA GAT ACT TTC CTC TTT AGA TAC Pro Ala Val Tyr Ala Lys Ala Tyr Glu Asp Thr Phe Leu Phe Arg Tyr 385 390 395 400	1200
AAT AGA TTA ATA TCC ATA AAT GAG GTT GGA AGC GAT TTA CGA TAT TAT Asn Arg Leu Ile Ser Ile Asn Glu Val Gly Ser Asp Leu Arg Tyr Tyr 405 410 415	1248
AAG ATA TCG CCT GAT CAG TTT CAT GTA TTT AAT CAA AAA CGA AGA GGA Lys Ile Ser Pro Asp Gln Phe His Val Phe Asn Gln Lys Arg Arg Gly 420 425 430	1296
AAA ATC ACA CTA AAT GCC ACT AGC ACA CAT GAT ACT AAG TTT AGT GAA Lys Ile Thr Leu Asn Ala Thr Ser Thr His Asp Thr Lys Phe Ser Glu 435 440 445	1344
GAT GTA AGG ATG AAA ATA AGT GTA TTA AGT GAA TTT CCT GAA GAA TGG Asp Val Arg Met Lys Ile Ser Val Leu Ser Glu Phe Pro Glu Glu Trp 450 455 460	1392
AAA AAT AAG GTC GAG GAA TGG CAT AGT ATC ATA AAT CCA AAG GTA TCA Lys Asn Lys Val Glu Glu Trp His Ser Ile Ile Asn Pro Lys Val Ser 465 470 475 480	1440
AGA AAT GAT GAA TAT AGA TAT TAT CAG GTT TTA GTG GGA AGT TTT TAT Arg Asn Asp Glu Tyr Arg Tyr Tyr Gln Val Leu Val Gly Ser Phe Tyr 485 490 495	1488
GAG GGA TTC TCT AAT GAT TTT AAG GAG AGA ATA AAG CAA CAT ATG ATA Glu Gly Phe Ser Asn Asp Phe Lys Glu Arg Ile Lys Gln His Met Ile 500 505 510	1536
AAA AGT GTC AGA GAA GCT AAG ATA AAT ACC TCA TGG AGA AAT CAA AAT Lys Ser Val Arg Glu Ala Lys Ile Asn Thr Ser Trp Arg Asn Gln Asn 515 520 525	1584
AAA GAA TAT GAA AAT AGA GTA ATG GAA TTA GTG GAA GAA ACT TTT ACC Lys Glu Tyr Glu Asn Arg Val Met Glu Leu Val Glu Glu Thr Phe Thr 530 535 540	1632

AAT AAG GAT TTC ATT AAA AGT TTC ATG AAA TTT GAA AGT AAG ATA AGA Asn Lys Asp Phe Ile Lys Ser Phe Met Lys Phe Glu Ser Lys Ile Arg 545 550 555 560	1680
AGG ATA GGG ATG ATT AAG AGC TTA TCC TTG GTC GCA TTA AAA ATT ATG Arg Ile Gly Met Ile Lys Ser Leu Ser Leu Val Ala Leu Lys Ile Met 565 570 575	1728
TCA GCC GGT ATA CCT GAT TTT TAT CAG GGA ACA GAA ATA TGG CGA TAT Ser Ala Gly Ile Pro Asp Phe Tyr Gln Gly Thr Glu Ile Trp Arg Tyr 580 585 590	1776
TTA CTT ACA GAT CCA GAT AAC AGA GTC CCA GTG GAT TTT AAG AAA TTA Leu Leu Thr Asp Pro Asp Asn Arg Val Pro Val Asp Phe Lys Lys Leu 595 600 605	1824
CAC GAA ATA TTA GAA AAA TCC AAA AAA TTT GAA AAA AAT ATG TTA GAG His Glu Ile Leu Glu Lys Ser Lys Lys Phe Glu Lys Asn Met Leu Glu 610 615 620	1872
TCT ATG GAC GAT GGA AGA ATT AAG ATG TAT TTA ACA TAT AAG CTT TTA Ser Met Asp Asp Gly Arg Ile Lys Met Tyr Leu Thr Tyr Lys Leu Leu 625 630 635 640	1920
TCC CTA AGA AAA CAG TTG GCT GAG GAT TTT TTA AAG GGC GAG TAT AAG Ser Leu Arg Lys Gln Leu Ala Glu Asp Phe Leu Lys Gly Glu Tyr Lys 645 650 655	1968
GGA TTA GAT CTA GAA GAA GGA CTA TGT GGG TTT ATT AGG TTT AAC AAA Gly Leu Asp Leu Glu Glu Gly Leu Cys Gly Phe Ile Arg Phe Asn Lys 660 665 670	2016
ATT TTG GTA ATA ATA AAA ACC AAG GGA AGT GTT AAT TAC AAA CTG AAA Ile Leu Val Ile Ile Lys Thr Lys Gly Ser Val Asn Tyr Lys Leu Lys 675 680 685	2064
CTT GAA GAG GGA GCA ATT TAC ACA GAT GTA TTG ACA GGA GAA GAA ATT Leu Glu Glu Gly Ala Ile Tyr Thr Asp Val Leu Thr Gly Glu Glu Ile 690 695 700	2112
AAA AAA GAG GTA CAG ATT AAT GAG CTA CCT AGG ATA CTA GTT AGA ATG Lys Lys Glu Val Gln Ile Asn Glu Leu Pro Arg Ile Leu Val Arg Met 705 710 715 720	2160

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 222 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GATCCGTTCT GGCAAATATT CTGAAATGAG CTGTTGACAA TTAATCATCG GCTCGTCTAA	60
TGTGTGGAAT TCTGATTCTGA ATTTTTTAAT AAAATCAGGA GGAAAAAATA TGATATCAGC	120
AACCTACAGA TTACAGTTAA ATAAGAATTT TAATTTTGGT GACGTAATCG ATGAATTCAC	180
TAGTTAGAAT GTGATGAAGG CCTGCGGCCG CTGCAGAGCT CA	222

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAYYTNTGGT AYTTYAARGA

20

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GARGARTGGC AYWSNATHAT

20

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GATCCGTTCT GGCAAATATT CTGAAATGAG CTGT

34

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGACAATTAA TCATCGGCTC GTCTAATGTG TGGAAATTCTG ATTCGA

46

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATTTTTTAAT AAAATCAGGA GGAAAAATA TGATATCAGC AACCTACA

48

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GATTACAGTT AAATAAGAAT TTTAATTTTG GTGACGTAAT CGATGAA

47

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTCACTAGTT AGAATGTGAT GAAGGCCTGC GGCCGCTGCA GAGCTCA

47

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CGATGATTAA TTGTCAACAG CTCATTTTCAG AATATTTGCC AGAAGC

46

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TTTTATTAAA AAATTCGAAT CAGAATTCCA CACATTAGAC GAGC

44

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TTAACTGTAA TCTGTAGGTT GCTGATATCA TATTTTTTCC TCCTGA

46

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TAGTGAATTC TACGATTACG TCACCAAAT TAAATTCTT AT

42

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AGCTTGAGCT CTGCAGCGGC CGCAGGCCTT CATCACATTC TAAC

44

665401-50661460